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Porcine Parainfluenza Virus Type 1 (PPIV-1) in U.S. Swine: Summary of Veterinary Diagnostic Laboratory Data

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Summary and Implications

Porcine Parainfluenza-1 (PPIV-1) is a Paramyxovirus in the genus *Respirovirus*. To evaluate the frequency of detection of PPIV-1 on farms in the United States, the Iowa State University Veterinary Diagnostic Laboratory (ISU VDL) conducted an analysis of clinical samples submitted from Spring to Fall 2016. Thirty-four percent of diagnostic samples tested both prospectively (70/204) and retrospectively (472/1385) were positive by polymerase chain reaction (PCR), which suggests PPIV-1 is widespread.

Introduction

PPIV-1 was first detected in swine at the University of Hong Kong in 2013, prompting diagnostic laboratories in the United States (US) to develop assays capable of detecting PPIV-1 in clinical samples. However, it is unclear whether PPIV-1 contributes significantly to the porcine respiratory disease complex (PRDC) since PPIV-1 has been detected from both symptomatic and asymptomatic herds. Other viruses comprising the PRDC include porcine reproductive and respiratory syndrome virus (PRRSV), porcine circovirus type 2 (PCV2) and influenza A virus (IAV). The pathogenesis, transmission, and epidemiology of PPIV-1 have yet to be determined.

Materials and Methods

Diagnostic samples submitted to the ISU VDL were tested prospectively and retrospectively by a PPIV-1-specific real time reverse transcriptase PCR (RT-rPCR). In total, 1589 samples collected from 27 US states were tested; these included but were not limited to oral fluid, tissue homogenates, environmental samples, serum, nasal swabs, oropharyngeal swabs, and bronchoalveolar lavage fluid.

Results and Discussion

A total of 34% of the clinical samples tested were RT-rPCR positive for PPIV-1 (Figure 1). These included oral fluid (75.4%), lung (7.2%), nasal swab (13.1%), and environmental samples (2.3%). These data suggest oral fluids are most likely to contain PPIV-1, followed distantly by nasal swabs.

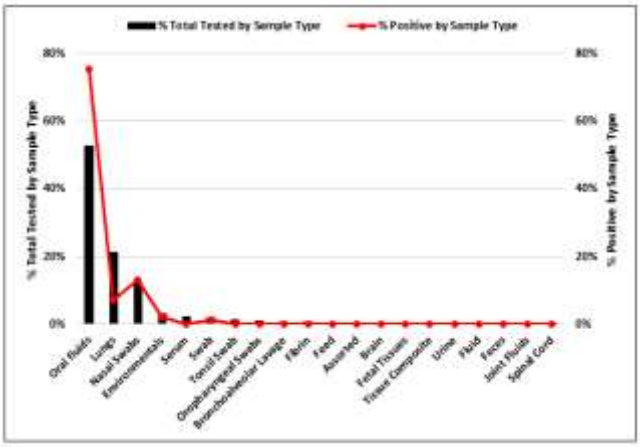

Figure 1: Percent of samples submitted to the ISU VDL with unknown clinical status and RT-rPCR positive for PPIV-1.

Iowa, North Carolina, and Illinois had the highest percent of PPIV-1 RT-rPCR positive samples by state, regardless of clinical history (Figure 2). This is correlated to the swine population distribution in the US and the relative proportion of samples submitted to the ISU VDL.

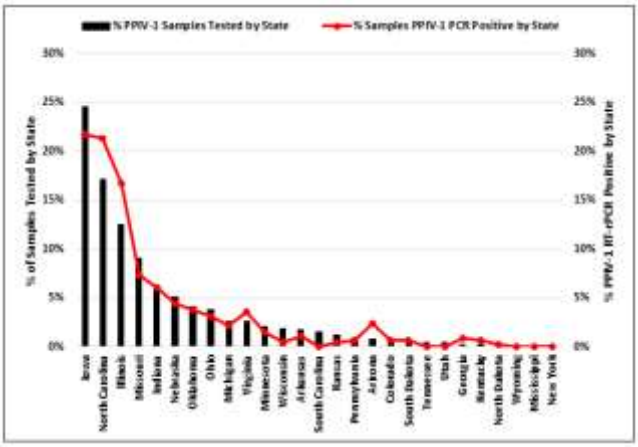

Figure 2: Diagnostic samples analyzed for PPIV-1 by state at the ISU VDL regardless of clinical history.

Among the cases in which clinical history suggests porcine respiratory disease is present, 49% of PPIV-1 RT-rPCR positive samples were nasal swabs, 7% oral fluid, and 20% other sample types. Even though PPIV-1 was detected most often in oral fluids, nasal swabs may be more

appropriate for PPIV-1 detection when associated with clinical disease (Figure 3).

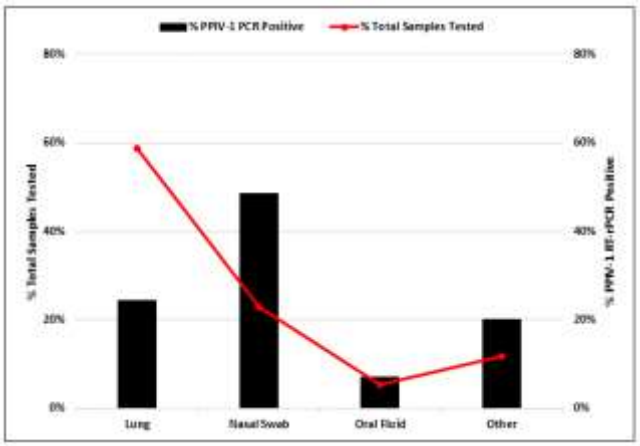

Figure 3: Percent of PPIV-1 positive accessions based on sample type and submitted to the ISU VDL with clinical history of respiratory disease

PPIV-1 was detected most often in nursery pigs, followed by grow-finish pigs. PPIV-1 was not commonly detected in suckling and adult pigs (Figure 4).

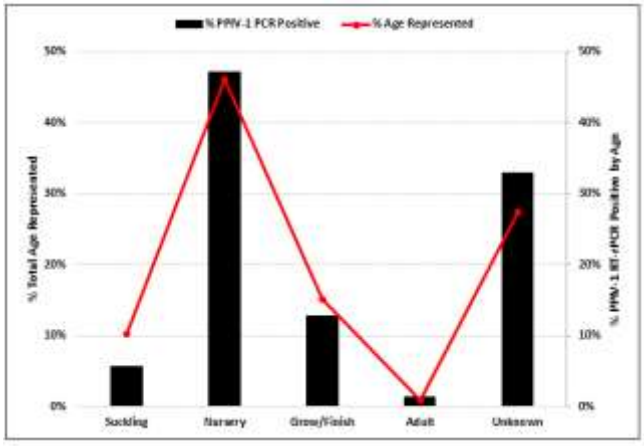

Figure 4: Percent of positive accessions based on age submitted to the ISU VDL with a clinical history of respiratory disease

PPIV-1 has also been detected in coinfections with IAV and PRRSV. Although it is still unknown, these viral coinfections could possibly increase severity of respiratory disease. In summary, these data suggest a high prevalence of PPIV-1 in US swine herds that may not be associated with clinical disease. Herds can be asymptomatic but still carry PPIV-1. More work is needed in developing a comprehensive diagnostic array of assays to assist in the detection of PPIV-1 as well as determining its contribution to the respiratory disease complex.

Acknowledgements

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